U.S. DEPARTMENT OF COMMERCE ATTY DOCKETNO APPLICATION NO FORM PTO-1449 PATENT AND TRADEMARK OFFICE ELITRA 0014 09/492,709 SUPPLEMENTAL INFORMATION DISCLOSURE STATEMENT BY APPLICANT APPLICANT Zyskind, **et** al (USE SEVERAL SHEETS IF NECESSARY) FILTING DATE GROUP Januar, 27, John 1631

				U.S. PATENT	DOCUMENTS			_				
EXAMINER: INITIAL		DOCUMENT NUMBER	DATE		NAME	CLASS	SUBCLASS	FILING (IF APPRO	SPOLATE			
AM	1	US 2002/0058260 A1	05.16.02	Zyskind, et al		435	6 RE	CEIV	FD			
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*EXAMINER: INITIAL IF CITATION CONSIDERED, WHETHER OR NOT CITATION IS A CONFORMANCE WITH MPEP 609, DRAW LINE THROUGH CITATION IF NOT IN CONFORMANCE AND NOT CONSIDERED, INCLUDE COPY OF THIS FORM WITH NEXT COMMUNICATION TO APPLICANT

SUPPLEMENTAL	ATTY, DOCKET NO. ELITRA.001A	APPLICATION NO 09/492,709
BY APPLICANT (USE SEVERAL SHEETS IF NECESSARY)	APPLICANT Zyskind, et al.	ŀ
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EXAMINER INITIAL		DOCUMENT NUMBER	DATE	NAME	CLASS	SUBCLASS	FILING (IF APPR	DATE OPRIATE)
AM	1	5,874,281	02/23/99	Dattagupta, et al.	435	238		
MM	2	5,874,567	02/23/99	Smith	536	24.5		
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FORM PTO-1449

U.S. DEPARTMENT OF COMMERCE PATENT AND TRADEMARK OFFICE

ATTY: DOCKET NO. ELITRA:001A APPLICATION NO 09/492,709

SUPPLEMENTAL INFORMATION DISCLOSURE STATEMENT BY APPLICANT

APPLICANT Zyskind, et al.

(USE SEVERAL SHEETS IF NECESSARY)

FILING DATE January 27, 2000 GROUP 1631

EKAMINER INITIAL		DOCUMENT NUMBER	DATE	NAME	CLASS	SUBCLASS	FILING DATE (IF APPROPRIATE
Am	1	6,228,579 B1	05/08/01	Zyskind, et al.	435	6	
AM	2	6,228,588 B1	05/08/01	Benton, et al.	435	6	
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E. AMINER	DOCUMENT NUMBER DATE		COUNTRY	CLASS	SUBCLASS	TRANSLATION	
INITIAL						YES	NO

EXAMINER INITIAL		OTHER DOCUMENTS (INCLUDING AUTHOR, TITLE, DATE, PERTINENT PAGES, ETC.)
AM	3	Good, et al. 1998. Inhibition of translation and bacterial growth by peptide nucleic acid targeted to ribosomal RNA. Proc. Natl. Acad. Sci. USA, 95:2073-2076
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SUPPLEMENTAL INFORMATION DISCLOSURE STATEMENT			
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U.S. PATENT DOCUMENTS							
EXAMINER INITIAL		DOCUMENT NUMBER	DATE	NAME	CLASS 3647	SUBCLASS	FILING DATE (IF APPROPRIATE)
AM	1	5,353,236	10/04/94	Subbiah I.			
sh	2	5,869,604	02/09/99	Rousseau, et al	530	344	
BM	3	6.077.682	06/20/00	Inouye, et al	439	15	
AM	4	6,156,526	12/05/00	Boriack-Sjodin, et al.	435	18	

FOREIGN PATENT DOCUMENTS								
EXAMINER	DOCUMENT NUMBER		DATE	COUNTRY	CLASS	SUBCLASS	TRANSLATION	
INITIAL							YES	NO
MW	5	WO 99/13893	03/25/99	PCT Nielsen ot al.				
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EXAMINER INITIAL			OTHER DOCUMENTS (INCLUDING AUTHOR, TITLE, DATE, PERTINENT PAGES, ETC.)			
SM		6	Appelt, K. 1993. Crystal structures of HIV-1 protease-inhibitor complexes. Perspectives in Drug Discovery and Design, 1 23-48.			
		7	Bagby, et al. 1994. Unusual helix-containing Greek keys in development-specific Ca ²⁺ -binding protein S. H. ¹⁵ N, and ¹³ C assignments and secondary structure determined with the use of multidimensional double and triple resonance heteronuclear NMR spectroscopy. <i>Biochemistry</i> , 33 2409-2421			
		8	Bagby, et al. 1995. Solution structure of the C-terminal core domain of human TFIIB: Similarity to Cyclin A and interaction with TATA-binding protein. <i>Cell</i> . 82:857-867.			
		9	Balbes, et al. 1994. "A perspective of modern methods in computer-aided drug design." In Lipkowitz, et al., Eds. Reviews in Computational Chemistry V. Chap. 7, pp. 337-379. New York: VCH Publishers			
		10,	Brunschwig, et al. 1992. A two-component T7 system for the overexpression of genes in <i>Pseudomonas aeruginosa. Gene.</i> 111 35-41			
 .	11		Bugg, et al. 1993. Drugs by design: Structure-based design, an innovative approach to developing drugs, has recently spawned many promising therapeutic agents, including several now inhuman trials for treating AIDS, cancer and other diseases. <i>Scientific American</i> , Dec. 92-98.			
		12.	Clore, et al. 1987. Three-dimensional structure of potato carboxypeptidase inhibitor in solution. A study using nuclear magnetic resonance, distance geometry, and restrained molecular dynamics. <i>Biochemistry</i> , 26.8012-8023.			
		13	Crosa, et al. 1973. Molecular relationships among the Salmonelleae. J. Bacteriol, 115(1):307-315			
			Cwirla, et al. 1990. Peptides on phage: A vast library of peptides for identifying ligands. Proc. Natl. Acad. Sci. USA, 87 6378-6382			
		15	Devlin, et al. 1990. Random peptide libraries: A source of specific protein binding molecules. Science, 249 404-406			
	1		Edwards, B. H. 1999. Salmonella and Shigella species. Clinics Lab. Med., 19(3) 469-487.			

EXAMINER	Ardn	Marschel	DATE CONSIDERED	12-20-02	

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(USE SEVERAL SHEETS IF NECESSARY)	FILING DATE January 27, 2000	GROUP 1631

EXAMINER INITIAL	OTHER DOCUMENTS (INCLUDING AUTHOR, TITLE, DATE, PERTINENT PAGES ETC.)						
Im	17 Erickson, J. W. 1993. Design and structure of symmetry-based inhibitors of HIV-1 protease. Perspectives in Drug Discovery and Design.						
1	18	Good, et al. 1998. Antisense inhibition of gene expression in bacteria by PNA targeted to mRNA. Nature Biotechinology, 16:355-358.					
1	19	Huycke, et al. 1998. Multiple-drug resistant enterococci: The nature of the problem and an agenda for the future. <i>Emerging Infectious Diseases</i> , 4(2):239-249.					
	20	Israelsen, et al. 1995. Cloning and partial characterization of regulated promoters from Lactococcus lactis Tn917-lacZ integrants with the new promoter probe vector, pAK80. Applied and Environmental Microbiology, 61(7):2540-2547.					
	21	k-reiswirth, et al. 1983. The toxic shock syndrome exotoxin structural gene is not detectably transmitted by a prophage. Nature, 305 709-712.					
	22	Lam. et al. 1994. Rational design of potent, bioavailable, nonpeptide cyclic ureas as HIV protease inhibitors. Science. 263 380-384					
	23	Marrone, et al. 2000 Discovering high-affinity ligands from the computationally predicted structures and affinities of small molecules bound to a target virtual screening approach. Perspectives in Drug Discovery and Design. 20 209-230					
	24	Mestres, et al. 2000. Similarity versus docking in 3D virtual screening. Perspectives in Drug Discovery and Design. 20:191-207					
	25	Mojumdar, et al. 1988. Characterization of the tetracycline resistance gene of plasmid pT181 of Staphylococcus aureus. J. Bacteriology, 170(12):5522-5528					
	26	Moszer, et al. 1995. SubtiList: A relational database for the Bacillus subtilis genome. Microbiology, 141 261-268					
	27	Moszer, I. 1998. The complete genome of Bacillus subtilis. From sequence annotation to data management and analysis. FEBS Letters, 430-28-36					
	28	Neidhardt, F. C. (Ed.) 1996. Escherichia coli and Salmonella. Cellular and molecular biology. 2nd Ed., Vol. 2, pp. 2269-2271. Washington, D.C. ASM Press					
	29	Schnappinger, et al. 1995. Extracellular expression of native human anti-lysozyme fragments in Staphylococcus carnosus. FEMS Microbiol. Let., 129:121-127.					
	30	Scott, et al. 1990. Searching for peptide ligands with an epitope library. Science, 249.386-390.					
	31	Shuker, et al. 1996. Discovering high-affinity ligands for proteins: SAR by NMR. Science, 274.1531-1534.					
	32	Suh, et al. 1995. Genetic and transcriptional organization of the <i>Bacillus subtilis spc-alpha</i> region. Database accession no. L47971 (ID. BSRPLP). >P002190118. •					
	33	Suh, et al. 1996. Genetic and transcriptional organization of the Bacillus subtilis spc-alpha region. Gene, 169:17-23.					
	34	Tatusov, et al. 2000. The COG database: A tool for genome-scale analysis of protein functions and evolution. <i>Nucleic Acids Research</i> , 28(1):33-36					
	35	Van Delden, et al. 1998. Cell-to-cell signaling and Pseudomonas aeruginosa infections. Emerging Infectious Diseases, 4(4) 551-560.					
	36	Wagner, et al. 1987. Protein structures in solution by nuclear magnetic resonance and distance geometry. The polypeptide fold of the basic pancreatic trypsin inhibitor determined using two different algorithms, DISGEO and DISMAN. J. Mol. Biol., 196:611-639.					
	37	Wlodawer, et al. 1993. Structure-based inhibitors of HIV-1 protease. <i>Annu. Rev. Biochem.</i> , 62 543-585.					
	38	Wüthrich, et al. 1983. Pseudo-structures for the 20 common amino acids for use in studies of protein conformations by measurements of intramolecular proton-proton distance constraints with nuclear magnetic resonance. J. Mol. Biol., 169:949-961.					
$\sqrt{}$	39	Xia, et al. 1999 Rapid method for the identification of essential genes in Staphylococcus aureus. Plasmid. 42.144-149					

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